

3101



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,800

DATE: 02/26/2002

TIME: 13:20:13

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5 <110> APPLICANT: Roschke, Viktor
6     Rosen, Craig A.
7     Ruben, Steven, M.
10 <120> TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
13 <130> FILE REFERENCE: 1488.115000I
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/067,800
C--> 15 <141> CURRENT FILING DATE: 2002-02-08
15 <150> PRIOR APPLICATION NUMBER: PCT/US01/04153
16 <151> PRIOR FILING DATE: 2001-02-09
18 <150> PRIOR APPLICATION NUMBER: 09/779,880
19 <151> PRIOR FILING DATE: 2001-02-09
21 <150> PRIOR APPLICATION NUMBER: 60/297,257
22 <151> PRIOR FILING DATE: 2001-06-12
24 <150> PRIOR APPLICATION NUMBER: 60/310,458
25 <151> PRIOR FILING DATE: 2001-08-08
27 <150> PRIOR APPLICATION NUMBER: 60/328,447
28 <151> PRIOR FILING DATE: 2001-10-12
30 <150> PRIOR APPLICATION NUMBER: 60/341,725
31 <151> PRIOR FILING DATE: 2001-12-21
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35 <170> SOFTWARE: PatentIn version 3.1
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41 <213> ORGANISM: Homo sapiens
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44 <221> NAME/KEY: CDS
45 <222> LOCATION: (259)..(1314)
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50 ggaagctagc agcaaacctt cccttcacta cgaaacttca ttgcttggcc caaaagagag      120
52 ttaattcaat gtagacatct atgtaggcaa ttaaaaaacct attgatgtat aaaacagttt      180
54 gcattcatgg agggcaacta aatacattct aggactttat aaaagatcac tttttattta      240
56 tgcacagggt ggaacaag atg gat tat caa gtg tca agt cca atc tat gac      291
57           Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
58           1           5           10
60 atc aat tat tat aca tcg gag ccc tgc cca aaa atc aat gtg aag caa      339
61 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
62           15           20           25
64 atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc atc ttt      387
65 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
66           30           35           40
68 ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac tgc caa      435

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69 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
70      45                      50                      55
72 agg ctg gag agc atg act gac atc tac ctg ctc aac ctg gcc atc tct      483
73 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
74 60                      65                      70                      75
76 gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tat gct gcc      531
77 Asp Leu Phe Phe Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
78      80                      85                      90
80 gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca ggg ctc      579
81 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu
82      95                      100                      105
84 tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc ctg aca      627
85 Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr
86      110                      115                      120
88 atc gat agg tac ctg gct atc gtc cat gct gtg ttt gct tta aaa gcc      675
89 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
90      125                      130                      135
92 agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg gtg gtg      723
93 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
94 140                      145                      150                      155
96 gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct caa aaa      771
97 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
98      160                      165                      170
100 gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt cag tat      819
101 Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
102      175                      180                      185
104 caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg ggg ctg      867
105 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
106      190                      195                      200
108 gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc cta aaa      915
109 Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
110      205                      210                      215
112 act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct gtg agg      963
113 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
114 220                      225                      230                      235
116 ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct ccc tac      1011
117 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
118      240                      245                      250
120 aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc ctg aat      1059
121 Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
122      255                      260                      265
124 aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg aca gag      1107
125 Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
126      270                      275                      280
128 act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat gcc ttt      1155
129 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
130      285                      290                      295
132 gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa aag cac      1203
133 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His

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136 att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa gag gct      1251
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138          320          325          330
140 ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag cag gaa      1299
141 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
142          335          340          345
144 ata tct gtg ggc ttg tgacacggac tcaagtgggc tgggtgacca gtcagagttg      1354
145 Ile Ser Val Gly Leu
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157 <400> SEQUENCE: 2
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161 Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
162          20          25          30
164 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
165          35          40          45
167 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg Leu Glu Ser Met
168          50          55          60
170 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
171 65          70          75          80
173 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
174          85          90          95
176 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
177          100          105          110
179 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
180          115          120          125
182 Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
183          130          135          140
185 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
186 145          150          155          160
188 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
189          165          170          175
191 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
192          180          185          190
194 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195          195          200          205
197 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
198          210          215          220
200 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
201 225          230          235          240
203 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
204          245          250          255
206 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser

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209 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
210          275          280          285
212 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
213          290          295          300
215 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
216 305          310          315          320
218 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
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239 <210> SEQ ID NO: 4
240 <211> LENGTH: 29
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244 <220> FEATURE:
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251 <210> SEQ ID NO: 5
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253 <212> TYPE: DNA
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283 <223> OTHER INFORMATION: 5' Oligonucleotide primer for HDGNR10
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 303 <212> TYPE: PRT
 304 <213> ORGANISM: Homo sapiens
 306 <400> SEQUENCE: 9

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310	Lys	Phe	Asp	Val	Lys	Gln	Ile	Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu	Tyr
311				20				25					30			
313	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	Leu	Val	Val	Leu
314			35				40					45				
316	Ile	Leu	Ile	Asn	Cys	Lys	Lys	Lys	Cys	Leu	Thr	Asp	Ile	Tyr	Leu	
317		50				55				60						
319	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Leu	Ile	Thr	Leu	Pro	Leu
320	65				70				75					80		
322	Trp	Ala	His	Ser	Ala	Ala	Asn	Glu	Trp	Val	Phe	Gly	Asn	Ala	Met	Cys
323				85				90					95			
325	Lys	Leu	Phe	Thr	Gly	Leu	Tyr	His	Ile	Gly	Tyr	Phe	Gly	Gly	Ile	Phe
326				100				105					110			
328	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala
329				115				120					125			
331	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	Gly	Val	Val	Thr	Ser
332		130				135						140				
334	Val	Ile	Thr	Trp	Leu	Val	Ala	Val	Phe	Ala	Ser	Val	Pro	Gly	Ile	Ile
335	145				150					155				160		
337	Phe	Thr	Lys	Cys	Gln	Lys	Glu	Asp	Ser	Val	Tyr	Val	Cys	Gly	Pro	Tyr
338				165				170					175			
340	Phe	Pro	Arg	Gly	Trp	Asn	Asn	Phe	His	Thr	Ile	Met	Arg	Asn	Ile	Leu
341				180				185					190			
343	Gly	Leu	Val	Leu	Pro	Leu	Leu	Ile	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile
344			195				200					205				
346	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala
347		210				215				220						
349	Val	Arg	Val	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Thr
350	225				230					235				240		
352	Pro	Tyr	Asn	Ile	Val	Ile	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly
353				245				250					255			
355	Leu	Ser	Asn	Cys	Glu	Ser	Thr	Ser	Gln	Leu	Asp	Gln	Ala	Thr	Gln	Val

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